

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior listings and versions thereof.

1. (Currently Amended) A method for transforming a ~~useful~~ plant by introducing a ~~gene of another species into the useful plant wherein the region of a factor relating to the poly (A) addition of the mRNA of the useful plant to be transformed contained in the base sequence of the gene of the other species is modified into another base sequence not relating to the poly (A) addition of the mRNA without substantially altering the function of the protein encoded by the gene to be introduced~~ heterologous nucleic acid encoding a protein, which comprises 1) identifying a polyadenylation signal sequence and a GT rich sequence in the heterologous nucleic acid wherein the polyadenylation signal sequence is selected from the group consisting of ATTTA, NATAAA, ANTAAA, AANAAA, AATNAA, AATANA, and AATAAN of which N is A, G, C or T and the GT rich sequence is 8 or more consecutive G and/or T nucleotides, 2) modifying the polyadenylation signal sequence and the GT rich sequence without altering the amino acid sequence of the protein encoded by the heterologous nucleic acid, 3) introducing the modified heterologous nucleic acid into the plant, and 4) expressing the modified heterologous nucleic acid in the plant.
2. (Currently Amended) The method according to claim 1, wherein the ~~gene of another species to be introduced~~ heterologous nucleic acid is derived from yeast.
3. (Cancelled)
4. (Currently Amended) The method according to ~~claim 3~~ claim 1, wherein the ~~region of a factor relating to the poly (A) addition of the mRNA is a base sequence having AATAAA like sequence~~ polyadenylation signal sequence is located in a downstream from the a GT rich base sequence.
5. (Currently Amended) The method according to ~~any one of claims 1-4~~ claim 1, wherein the modification of ~~base sequence in the region of a factor relating to the poly (A) addition of the mRNA~~ the polyadenylation signal sequence and the GT rich sequence is performed based on a codon usage of the plant to be transformed.

6. (Cancelled)
7. (Cancelled)
8. (Currently Amended) The method according to ~~any one of claims 1-7~~ claim 1, wherein the modification of ~~base sequence~~ the polyadenylation signal sequence is performed so as not to have an ATTTA sequence.
9. (Currently Amended) The method according to ~~any one of claims 1-8~~ claim 1, characterized by having a Kozak sequence ~~in the~~ upstream of the initiation codon of the ~~gene to be introduced~~ heterologous nucleic acid.
10. (Currently Amended) The method according to ~~any one of claims 1-9~~ claim 1, wherein the ~~gene to be introduced~~ heterologous nucleic acid encodes a protein involved in absorption of nutrition nutrients.
11. (Currently Amended) The method according to claim 10, wherein the ~~gene to be introduced is the gene encoding~~ heterologous nucleic acid encodes a ferric-chelate reductase FRE1.
12. (Currently Amended) The method according to claim 11, wherein the ~~gene~~ heterologous nucleic acid encoding ferric-chelate reductase FRE1 is derived from yeast.
13. (Currently Amended) The method according to ~~any one of claims 1-12~~, claim 1 wherein the ~~useful~~ plant is grass germinaeae.
14. (Currently Amended) The method according to ~~any one of claims 1-12~~, claim 1 wherein the ~~useful~~ plant is tobacco.
15. (Currently Amended) A transformed ~~useful~~ plant which can be produced by the method according to ~~claims 1-14~~ claim 1.
16. (Currently Amended) A seed produced by the plant according to claim 15 ~~wherein the plant is seed~~.